Please *consult* *Sequence* *Rules* *for* *valid* *format*

1600

```
                RAW SEQUENCE LISTING            DATE: 10/18/2002
                PATENT APPLICATION:  US/09/487,790    TIME: 10:12:02

                Input Set : A:\EP.txt
                Output Set: N:\CRF4\10182002\I487790.raw
```

Does Not Comply
Corrected Diskette Needed

```
                SEQUENCE LISTING
C-->   3 (1) GENERAL INFORMATION:
       4      (i) APPLICANT: HADASIT MEDICAL RESEARCH SERVICES AND DEVLOPMENT COMPANY
       5              LTD.
       6     (ii) TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
       7    (iii) NUMBER OF SEQUENCES: 12
C-->   9     (vi) CURRENT APPLICATION DATA:
C--> 10          (A) APPLICATION NUMBER: US/09/487,790
C--> 11          (B) FILING DATE: 20-Jan-2000
     12          (C) CLASSIFICATION:
     13    (vii) PRIOR APPLICATION DATA:
     14          (A) APPLICATION NUMBER:
     15          (B) FILING DATE:
```

see pp 1-3

```
(vi) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE:
    (B) STREET:
    (C) CITY:
    (D) STATE:
    (E) COUNTRY:
    (F) ZIP:
(vii) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE:
    (B) COMPUTER:
    (C) OPERATING SYSTEM:
    (D) SOFTWARE:
```

insert these mandatory headings and responses for a U.S. application

FYI: all U.S. applications which do not have a prior application filed before July 1, 1998, need to be in "new" Sequence Rules format

```
ERRORED SEQUENCES                                1
```
use the numeral "1" not letter "l"

```
E--> 17 (2) INFORMATION FOR SEQ ID NO: 1:
     18      (i) SEQUENCE CHARACTERISTICS:
     19          (A) LENGTH: 21
     20          (B) TYPE: amino acid
     21          (C) STRANDEDNESS: single
     22          (D) TOPOLOGY: linear
C--> 23     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     24 Lys Gly Ser Trp Tyr Ser Met Arg Lys Met Ser Met Lys Ile Arg Pro Phe Phe Pro
E--> 25 Glu Glu
     26 (2) INFORMATION FOR SEQ ID NO: 2:
     27      (i) SEQUENCE CHARACTERISTICS:
     28          (A) LENGTH: 21
     29          (B) TYPE: amino acid
     30          (C) STRANDEDNESS: single
     31          (D) TOPOLOGY: linear
     32     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 33 Lys Thr Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn Arg
E--> 34 Leu Thr
     35 (2) INFORMATION FOR SEQ ID NO: 3:
     36      (i) SEQUENCE CHARACTERISTICS:
     37          (A) LENGTH: 20
     38          (B) TYPE: amino acid
     39          (C) STRANDEDNESS: single
     40          (D) TOPOLOGY: linear
     41     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 42 Arg Gly Ala Asp Tyr Ser Leu Arg Ala Val Arg Met Lys Ile Arg Pro Leu Val Thr
```

Per Sequence Rules A MAXIMUM of 16 amino acids per line → insert hard return

number the amino acids under every 5 amino acids (see Error Summary Sheet) (GLOBAL ERROR) use letter "l", do not use numeral "1"

1   5   10   15

invalid

same error as above

invalid *Ile?*

RAW SEQUENCE LISTING   DATE: 10/18/2002
PATENT APPLICATION: US/09/487,790   TIME: 10:12:02   **RECEIVED**

Input Set : **A:\EP.txt**   OCT 2 5 2002
Output Set: **N:\CRF4\10182002\I487790.raw**

                                                                   TECH CENTER 1600/2900

```
E--> 43 Glu
     53 (2) INFORMATION FOR SEQ ID NO: 5:
     54       (i) SEQUENCE CHARACTERISTICS:
     55           (A) LENGTH: 20
     56           (B) TYPE: amino acid                    same error
     57           (C) STRANDEDNESS: single
     58           (D) TOPOLOGY: linear
     59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 60 Leu Thr (Ile) Gly Glu Gly Glu Glu His His Leu Gly Gly Ala Lys Glu Ala Gly Asp
E--> 61 Val        Ile ?
C--> 62 (2)-INFORMATION FOR SEQ ID NO: 6:                                      one
     63       ↑ (i) SEQUENCE CHARACTERISTICS:                          space between
     64 delete     (A) LENGTH: 29                    same error       ✓ amino acids
     65 dash        (B) TYPE: amino acid
     66           (C) STRANDEDNESS: single
     67           (D) TOPOLOGY: linear
     68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 69 (X  X) Gly Val Val Trp (X X X X) Gly (X X) Tyr Ser (X) Arg (X X X) Met (Ly) Invalid
E--> 70 Ile Arg Pro (X X X) Glu                                 do you mean Xaa? "X" is
     72 (2) INFORMATION FOR SEQ ID NO: 7:                              invalid
     73       (i) SEQUENCE CHARACTERISTICS:
     74           (A) LENGTH: 65
     75           (B) TYPE: nucleic acid
     76           (C) STRANDEDNESS: double
     77           (D) TOPOLOGY: linear
     78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 79 AAGGGGTCATGGTATCAATGAGGAAGATGAGTATGAAGATCAGGCCCTTCTTCCCACAGCAATAG    invalid. Per
     81 (2) INFORMATION FOR SEQ ID NO: 8:                                     sequence
     82       (i) SEQUENCE CHARACTERISTICS:                                    Rules,
     83           (A) LENGTH: 63                                               group all
     84           (B) TYPE: nucleic acid                                       non-coding
     85           (C) STRANDEDNESS: double                                     nucleotides
     86           (D) TOPOLOGY: linear              same errors                into 10's,
     87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 88 AGAGGGGCAGATTATTCCCTCAGGGCTGTTCGCATGAAAATTAGGCCCCTTGTGACCCAATAG             with a (one)
     90 (2) INFORMATION FOR SEQ ID NO: 9:                                        space
     91       (i) SEQUENCE CHARACTERISTICS:                                      between
     92           (A) LENGTH: 63                                                 each
     93           (B) TYPE: nucleic acid                                         group
     94           (C) STRANDEDNESS: double           same
     95           (D) TOPOLOGY: linear
     96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 97 AAAACCCGGTGGTATTCCATGAAGAAAACCACTATGAAGATAATCCCATTCAACAGACTCACA
     99 (2) INFORMATION FOR SEQ ID NO: 10:          Insert cumulative
    100       (i) SEQUENCE CHARACTERISTICS:          base total at right
    101           (A) LENGTH: 15                      margin of each line
    102           (B) TYPE: amino acid
    103           (C) STRANDEDNESS: single
    104           (D) TOPOLOGY: linear
```

use numeral "0"
NOT letter "O"

file://C:\CRF4\Outhold\VsrI487790.htm   10/18/02

RAW SEQUENCE LISTING   DATE: 10/18/2002
PATENT APPLICATION: US/09/487,790   TIME: 10:12:02

Input Set : A:\EP.txt
Output Set: N:\CRF4\10182002\I487790.raw

[handwritten: same error as previous pages]

```
       105      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10
E-->   106 Tyr Ser (X) Arg (X X) Met Lys (IIe) Arg Pro (X X X) Glu
C-->   108 (2) INFORMATION FOR SEQ ID NO: (11)
       109     (i) SEQUENCE CHARACTERISTICS:
       110         (A) LENGTH: 20
       111         (B) TYPE: amino acid
       112         (C) STRANDEDNESS: single
       113         (D) TOPOLOGY: linear
E-->   114      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E-->   115 Lys (X X) Trp Tyr Ser Met (X) Lys (X X) Met Lys (IIe)(X) Pro Phe (X X X)
E-->   117 (2) INFORMATION FOR SEQ ID NO: (12):
       118     (i) SEQUENCE CHARACTERISTICS:
       119         (A) LENGTH: 30
       120         (B) TYPE: amino acid
       121         (C) STRANDEDNESS: single
       122         (D) TOPOLOGY: linear
E-->   123      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12
E-->   124 Asp (X) Gly (X X) Trp (X X) Trp Lys (X X) Trp Tyr Ser Met (X) Lys (X X) Met Lys Ile (X)
E-->   125 Pro Phe (X X X)
E-->   130 (1)
```

[handwritten annotations: Ile? ; same error ; use Xaa ; use numbers, not letters ; insert ; colon ; Ile? ; number "1" ; use number "1" same ; delete]

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/18/2002
PATENT APPLICATION: **US/09/487,790**   TIME: 10:12:03

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10182002\I487790.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:6; Line(s) 69

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/487,790**

DATE: 10/18/2002
TIME: 10:12:03

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10182002\I487790.raw**

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:9 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:10 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:11 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)
L:17 M:202 E: (16) Value must be an Integer, Data=[1:]
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, Value=[1:]
L:25 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:33 M:330 E: (2) Invalid Amino Acid Designator, 2
L:34 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:42 M:330 E: (2) Invalid Amino Acid Designator, 1
L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:60 M:330 E: (2) Invalid Amino Acid Designator, 1
L:61 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:62 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:69 M:330 E: (2) Invalid Amino Acid Designator, 13
L:70 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:70 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:70 M:330 E: (2) Invalid Amino Acid Designator, 3
L:79 M:254 E: No. of Bases conflict, Input:0 Counted:65 SEQ:7
L:88 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:8
L:97 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:9
L:106 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:106 M:330 E: (2) Invalid Amino Acid Designator, 7
L:108 M:202 E: (16) Value must be an Integer, Data=[11]
L:108 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:114 M:202 E: (16) Value must be an Integer, Data=[11:]
L:115 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:115 M:330 E: (2) Invalid Amino Acid Designator, 10
L:117 M:202 E: (16) Value must be an Integer, Data=[12]
L:123 M:202 E: (16) Value must be an Integer, Data=[12]
L:124 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:124 M:330 E: (2) Invalid Amino Acid Designator, 11
L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:125 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:125 M:330 E: (2) Invalid Amino Acid Designator, 4
M:332 Repeated in SeqNo=-1

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

Please note

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.